

IAP5 Rec'd PCT/PTO 27 SEP 2006

## SEQUENCE LISTING

&lt;110&gt; POSTECH FOUNDATION, et al.

&lt;120&gt; Flowering time-controlling gene COG2 isolated from Arabidopsis thaliana

&lt;130&gt; PCA50313-PSC

&lt;150&gt; KR 10-2004-0021216

&lt;151&gt; 2004-03-29

&lt;160&gt; 8

&lt;170&gt; KopatentIn 1.71

&lt;210&gt; 1

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 1

```

atggcgactc aagattctca agggattaaa ctctttggca aaactattgc atttaacact      60
cgaacaataa aaaatgaaga agagacacac ccgccggagc aagaagccac aatagccgtt      120
agatcatcat catcatcgga tctgacggcc gagaagcgtc cggataagat catagcatgt      180
ccaagatgca agagcatgga gacaaagttc tgttacttca acaactacaa cgtaaatcag      240
cctcgacact ttigttaaagg ctgccaccgt tactggaccg ccggtggtgc actccggaac      300
gttcccgtcg gcgccggtcg tcggaagtcc aaaccacctg gtcgtgtcgt ggttggtatg      360
cttggagatg gaaatggtgt tcgccaagtc gagcttataa atggcttgct cgttgaggag      420
tggcagcatg ccgcagccgc agctcacggt agtttcgggc atgattttcc catgaagcgg      480
ctccggtggt actccgacgg tcaatcgtgc tga                                     513

```

&lt;210&gt; 2

&lt;211&gt; 170

<212> PRT  
 <213> Arabidopsis thaliana

<220>  
 <221> SIGNAL  
 <222> (107)..(111)  
 <223> Nucleus localization signal

<400> 2

```

Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile
  1           5           10          15
Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro
          20          25          30
Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
          35          40          45
Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
          50          55          60
Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Val Asn Gln
          65          70          75          80
Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
          85          90          95
Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
          100         105         110
Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg
          115         120         125
Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala
          130         135         140
Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg
          145         150         155         160
Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys
          165         170

```

<210> 3  
 <211> 528  
 <212> DNA  
 <213> Arabidopsis thaliana

&lt;400&gt; 3

```

atggcgaccc aagattctca agggattaaa ctctttggca aaaccataac attcaacgcc      60
aacatcacac agacgataaa aaaagaagag cagcaacaac aacaacagcc agagctacaa      120
gcaacaacag ccgttagatc accctcatcg gatctgacgg ctgagaagcg tccagacaag      180
atcataccat gtccgagatg caagagcatg gagactaagt ttgttactt caacaactac      240
aacgttaatc aaccaagaca ctcttgcaaa ggttgtcaac gtactggac cgccggtgga      300
gctctccgga atgttcccggt cggtgccggt cgtcggaagt caaaacctcc cggacgtgtc      360
ggtagggttcg ctgagttgct tggagctgcg actggagctg ttgatcaggt cgagctagat      420
gctttgctag tggaagagtg gagagctgct acggcgtctc acggtgggtt ccggcatgat      480
ttccggtga agaggctccg ttgttacacc gatggccaat cttgttaa      528

```

&lt;210&gt; 4

&lt;211&gt; 175

&lt;212&gt; 5n.

<213> *Arabidopsis thaliana*

&lt;400&gt; 4

```

Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile
 1           5           10           15
Thr Phe Asn Ala Asn Ile Thr Gln Thr Ile Lys Lys Glu Glu Gln Gln
      20           25           30
Gln Gln Gln Gln Pro Glu Leu Gln Ala Thr Thr Ala Val Arg Ser Pro
      35           40           45
Ser Ser Asp Leu Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Pro Cys
      50           55           60
Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr
      65           70           75           80
Asn Val Asn Gln Pro Arg His Phe Cys Lys Gly Cys Gln Arg Tyr Trp
      85           90           95
Thr Ala Gly Gly Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg
      100          105          110
Lys Ser Lys Pro Pro Gly Arg Val Gly Gly Phe Ala Glu Leu Leu Gly
      115          120          125
Ala Ala Thr Gly Ala Val Asp Gln Val Glu Leu Asp Ala Leu Leu Val
      130          135          140

```

Glu Glu Trp Arg Ala Ala Thr Ala Ser His Gly Gly Phe Arg His Asp  
 145 150 155 160

Phe Pro Val Lys Arg Leu Arg Cys Tyr Thr Asp Gly Gln Ser Cys  
 165 170 175

<210> 5  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> forward primer specific for COG2

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> NcoI restriction site

<400> 5  
 ccatggccat tctctgcacg ttctc

25

<210> 6  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> reverse primer specific for COG2

<220>  
 <221> misc\_feature  
 <222> (1)..(7)  
 <223> BstEII restriction site

&lt;400&gt; 6

ggtnacctca gcacgattga ccg

23

&lt;210&gt; 7

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; forward primer specific for ACT8

&lt;400&gt; 7

aatcagatgt ggatctctaa ggca

24

&lt;210&gt; 8

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; reverse primer specific for ACT8

&lt;400&gt; 8

tccgagtttg aagaggctac aaac

24